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Genetic characterization of canine distemper virus involved in outbreaks in farmed mink in Denmark 2012

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Danish farmed mink herds experienced a large outbreak of canine distemper virus in 2012. Full-length sequence analysis (1824 nucleotides) of the variable hemagglutinin (H) gene were performed on 27 viruses collected from mink and on 7 viruses collected from wild foxes. Results of the study showed that the farmed mink and wild fox population were infected by identical viruses which strongly indicate an epidemiological link between these populations. Accordingly, diseased and dead foxes were observed in some of the mink herds in connection to the outbreak. The Danish virus strain clustered phylogenetically with other European canine distemper viruses and showed the highest level of similarity (99.3 - 99.6 %) to viruses isolated from wild foxes in Germany. The fox should therefore be considered as an important wild life reservoir of canine distemper virus and may also contribute to the transmission of the virus between mink farms during outbreaks.